

SEQUENCE LISTING



<110> GONG, Zhiyuan
LAM, Toong Jin
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<120> CHIMERIC GENE CONSTRUCTS FOR GENERATION OF FLUORESCENT
TRANSGENIC ORNAMENTAL FISH

<130> 1781-0163P

<140> 09/913,898

<141> 2001-08-17

<150> PCT/SG99/00079

<151> 1999-01-14

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<170> PatentIn Ver. 2.0

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Arg Ser Gly Val Gly Ala Ser Pro Gly Phe Gly Ala Gly Gly Ser Tyr
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Ser Phe Ser Ser Ser Ser Met Gly Gly Gly Tyr Gly Ser Gly Leu Gly
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Gly Gly Leu Gly Gly Gly Met Gly Phe Arg Cys Gly Leu Pro Ile Thr
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gct gta act gtc aac cag aac ctg ttg gcc ccc tta aac ctg gaa atc 401
Ala Val Thr Val Asn Gln Asn Leu Leu Ala Pro Leu Asn Leu Glu Ile
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Gln Thr Thr Thr Arg Ser Asn Ile Asp Ala Met Phe Glu Ala Tyr Ile
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Gly Gly Tyr Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly Gly Met Gly
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Phe Arg Cys Gly Leu Pro Ile Thr Ala Val Thr Val Asn Gln Asn Leu
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Leu Ala Pro Leu Asn Leu Glu Ile Asp Pro Thr Ile Gln Ala Val Arg
 100 105 110

Thr Ser Glu Lys Glu Gln Ile Lys Thr Phe Asn Asn Arg Phe Ala Phe
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Leu Ile Asp Lys Val Arg Phe Leu Glu Gln Gln Asn Lys Met Leu Glu
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 Asp Ala Met Phe Glu Ala Tyr Ile Ser Asn Leu Arg Arg Gln Leu Asp
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 Gly Leu Gly Asn Glu Lys Met Lys Leu Glu Gly Glu Leu Lys Asn Met
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 Gln Gly Leu Val Glu Asp Phe Lys Asn Lys Tyr Glu Asp Glu Ile Asn
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 Lys Arg Ala Ser Val Glu Asn Glu Phe Val Leu Leu Lys Lys Asp Val
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 Asp Ala Ala Tyr Met Asn Lys Val Glu Leu Glu Ala Lys Val Asp Ala
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 Trp Tyr Lys Gln Lys Phe Glu Glu Met Gln Ser Thr Ala Gly Gln Tyr
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 Lys Leu Leu Glu Gly Glu Glu Ser Arg Leu Ser Ser Gly Gly Ala Gln
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 Ala Thr Ile His Val Gln Gln Thr Ser Gly Gly Val Ser Ser Gly Tyr
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Met Pro Phe Gly Asn Thr His Asn Asn
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ttc aag ctg aac tac tca gtt gat gag gag tat cca gac ctt agc aag 160
Phe Lys Leu Asn Tyr Ser Val Asp Glu Glu Tyr Pro Asp Leu Ser Lys
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cac aac aac cac atg gcc aag gtg ctg act aag gaa atg tat ggc aag 208
His Asn Asn His Met Ala Lys Val Leu Thr Lys Glu Met Tyr Gly Lys
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ctt agg gac aag cag acc cca cct gga ttc act gtg gat gat gtc atc 256
Leu Arg Asp Lys Gln Thr Pro Pro Gly Phe Thr Val Asp Asp Val Ile
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cag act ggt gtt gac aat cca ggc cac ccc ttc atc atg acc gtc ggc 304
Gln Thr Gly Val Asp Asn Pro Gly His Pro Phe Ile Met Thr Val Gly

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Cys Val Ala Gly Asp Glu Glu Ser Tyr Asp Val Phe Lys Asp Leu Phe			
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His Lys Thr Asp Leu Asn Phe Glu Asn Leu Lys Gly Gly Asp Asp Leu			
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Val Glu Lys Leu Ser Val Glu Ala Leu Ser Ser Leu Asp Gly Glu Phe			
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Gln Leu Ile Ala Asp His Phe Leu Phe Asp Lys Pro Val Ser Pro Leu			
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Leu Leu Ala Ala Gly Met Ala Arg Asp Trp Pro Asp Ala Arg Gly Ile			
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Trp His Asn Glu Asn Lys Ala Phe Leu Val Trp Val Lys Gln Glu Asp			
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His Leu Arg Val Ile Ser Met Gln Lys Gly Gly Asn Met Lys Glu Val			
	235	240	245
ttc aag cgc ttc tgc gtt ggt ctt cag agg att gag gaa att ttc aag			880
Phe Lys Arg Phe Cys Val Gly Leu Gln Arg Ile Glu Glu Ile Phe Lys			
	250	255	260
aag cac aac cat ggg ttc atg tgg aac gag cat ctt ggt ttc gtc ctg			928
Lys His Asn His Gly Phe Met Trp Asn Glu His Leu Gly Phe Val Leu			
	270	275	280
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Thr Cys Pro Ser Asn Leu Gly Thr Gly Leu Arg Gly Gly Val His Val			
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 Glu Val Glu Gln Val Gln Cys Val Val Asp Gly Val Lys Leu Met Val
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 Pro Ala Gln Lys
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Pro Gly Phe Thr Val Asp Asp Val Ile Gln Thr Gly Val Asp Asn Pro
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Gly His Pro Phe Ile Met Thr Val Gly Cys Val Ala Gly Asp Glu Glu
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Ser Tyr Asp Val Phe Lys Asp Leu Phe Asp Pro Val Ile Ser Asp Arg
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His Gly Gly Tyr Lys Ala Thr Asp Lys His Lys Thr Asp Leu Asn Phe
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Glu Asn Leu Lys Gly Gly Asp Asp Leu Asp Pro Asn Tyr Phe Leu Ser
115 120 125

Ser Arg Val Arg Thr Gly Arg Ser Ile Lys Gly Tyr Pro Leu Pro Pro
130 135 140

His Asn Ser Arg Gly Glu Arg Arg Ala Val Glu Lys Leu Ser Val Glu
145 150 155 160

Ala Leu Ser Ser Leu Asp Gly Glu Phe Lys Gly Lys Tyr Tyr Pro Leu
165 170 175

Lys Ser Met Thr Asp Asp Glu Gln Glu Gln Leu Ile Ala Asp His Phe
180 185 190

Leu Phe Asp Lys Pro Val Ser Pro Leu Leu Leu Ala Ala Gly Met Ala
195 200 205

Arg Asp Trp Pro Asp Ala Arg Gly Ile Trp His Asn Glu Asn Lys Ala
210 215 220

Phe Leu Val Trp Val Lys Gln Glu Asp His Leu Arg Val Ile Ser Met
225 230 235 240

Gln Lys Gly Gly Asn Met Lys Glu Val Phe Lys Arg Phe Cys Val Gly
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Leu Gln Arg Ile Glu Glu Ile Phe Lys Lys His Asn His Gly Phe Met
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Trp Asn Glu His Leu Gly Phe Val Leu Thr Cys Pro Ser Asn Leu Gly
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Thr Gly Leu Arg Gly Gly Val His Val Lys Leu Pro Lys Leu Ser Thr
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 Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Phe Pro Lys Cys Phe
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ctg tcc ctg cgg ggc aag gcc gtc gtg ctc atg ggg aaa aac acc atg 254
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atg agg aag gcc att cgt ggc cac ctg gaa aac aac cca gct ctg gag 302
 Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu
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 Arg Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys
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 Glu Asp Leu Thr Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro
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 Asp Val Gln Leu Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala
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 Glu Val Leu Asp Ile Thr Glu Asp Ala Leu His Lys Arg Phe Leu Lys
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 Ala Val Thr Val Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val
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 Lys Ala Tyr Leu Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val
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Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
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Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Arg Leu Leu Pro
65 70 75 80

His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
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Glu Val Arg Asp Leu Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
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Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
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Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
130 135 140

Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
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Ile Lys Pro Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
165 170 175

Met Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Tyr Gly Leu Ile Ile
180 185 190

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195 200 205

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210 215 220

Ile Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Leu Ala Ser Ile
225 230 235 240

Pro His Thr Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Val Thr Val
245 250 255

Glu Thr Asp Tyr Thr Phe Pro Leu Ala Glu Lys Val Lys Ala Tyr Leu
260 265 270

Ala Asp Pro Thr Ala Phe Ala Val Ala Ala Pro Val Ala Ala Ala Thr
275 280 285

Glu Gln Lys Ser Ala Ala Pro Ala Ala Lys Glu Glu Ala Pro Lys Glu
 290 295 300

Asp Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
 305 310 315

<210> 7
 <211> 2241
 <212> DNA
 <213> Danio rerio

<220>
 <221> TATA signal
 <222> (2103)..(2108)

<220>
 <221> primer_bind
 <222> (2221)..(2241)
 <223> CK2

<220>
 <221> misc_feature
 <222> (2142)..(2235)
 <223> Identical to the 5' CK cDNA

<400> 7
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 gattactcat ctcaaacacc catacaaagg gatgattgcc gtaccatgat ctcacacctt 120
 tcacacctgg ttatactat gatagttgta gacgattgcg taatgctatt aaatgcccat 180
 cagtgtctggc tgtgacaccc aactgctgcc atttcgtgtt gacttgcacg agaaatgaga 240
 aattgtctga ctatgcaggg tgtctatgcg tgggaacatt tatcagtggt cattaaatac 300
 tatagtttac agttagacca aagtgtgctg tatttttgtg ttagcttagc tgcagttttt 360
 gtgtgtgaag taacaaatga caaataactca aactattgta attaaagtag ttttctcaga 420
 aattgtaatt tactaagtag tttaaaaatg tgtactttta ctttcccttg agtacatttt 480
 tagtgcagtg ttggtacttt tatttcaactt ccttcccttca acctgcagtc actactttat 540
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 acatagaagg taaatcacat cataatgaac taccttaaga catgggccat ttataattgc 660
 agcaaaactgt ttgccagcat taaaagaaga tgtcaaaaat atttacacgc attaacccag 720
 agactgctta gatgcatgac actgatgaga agatgatgga tgtttactgt atgatgaccg 780
 aaataacttt aaacgcacac aagacggcac aagacgtcaa catggcgtaa ggttgacgtt 840
 gtacccaac gcagtgggga cggtgcattt tgtttagaaa tgaaaattag gttgacgtca 900
 gaactcaacg tcaggtcgat gtcaatgttc aacatccaat ctaaaatcat atatcaatgt 960
 ctaatgatgt tacagcttga tgttatgcgg atgttacctt tatgacgtct atcagacgtt 1020
 ggattatggt tgccatacct gatgaataaa tgtcattatt tgacgttggg ttaagatggt 1080
 ggttcgacat tggatttttg tgcgtttcca acacaacctt aatccaccaa atattaactt 1140
 cctatgacat cgttattgga cgtcaaaaata acaatatcct tagatgctgg ctgacttttg 1200
 aatttaggtc accacaacct atatttaacc taatattaac atcttatgat gttgtgtgcc 1260
 tgctgggcaa taactaaatg cactacagaa tgttacgttt acacacatgt aaattacatg 1320
 taaatgcatc agcttttcac agcataatac tcactactta ctactcttga gtacttttaa 1380
 aaaagctact tttcaactcat actttgagta atattttaca ctgatacttt tactcgcact 1440
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 cagccctccc catacataat cgtatgttta cacatatggt ggagtttaga gccataatct 1560
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 atatcaatac agaaggaaac tgtgttcctt gttcccttgt aaatctcaac aatgcaactg 1680
 ttcagctcag ggggaaaaat gccctgccag atccaaacgg ctggcaaaaag tgaatggaaa 1740
 aaagcctttc attaatgtga aagttgctgc gcgccccacc cagataaaaa gagcagaggt 1800

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taacatgctc tctacggctg tccagccaac cagatactga ggcagaaaca caccgcgtgg 1860
cagatgggtga gagctacact gtcttttcca gagtttctac tggaatgcct gtcctcaagt 1920
ctcaagcctc tccttgcatc ctctcattcc acctggggca aagccccagg ctgggtgtga 1980
caacatttat cttaccactt tctctctgta cctgtctaac aggtagggtg tgtgtgagag 2040
tgcgatatgt tgcaagtgcg tgtgtgtgtg agagcagtcg gctccaccct ctcaagagt 2100
tgtataaaat tggtcagcca gctgctgaga gacacgcaga gggactttga ctctcctttg 2160
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actcaaagac acaggatccg g 2241

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<210> 8
<211> 1456
<212> DNA
<213> Danio rerio

```

```

<220>
<221> TATA_signal
<222> (1389)..(1394)

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```

<220>
<221> primer_bind
<222> (1433)..(1456)
<223> MCK2

```

```

<220>
<221> misc_feature
<222> (1428)..(1453)
<223> Identical to the 5' MCK cDNA

```

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<400> 8
gaattgcaaa gtcagagtaa taaaatgaaa ccaaaaaaca tttttaaata tacttgtctc 60
tgtggcttaa tcttggctga tgtgtgtgtg tgtgtgtgtg tacttgacag ctgctagtga 120
gcatgtgcac catgacaggc ctgttattca cacttgggtg catgttggag actgttcggc 180
cagctatagt tttcttcaca gagtcctggg tcacctaatg tcacaaggaa gaaacatgtt 240
acatgttaaa atgtgacatt caaattgtag tgcattactt aacgaaacgc attacacaag 300
ttacagctta aaagattgct agacagaaaa accaggggagg ggttttccca taatatccag 360
tgagactcta ggagcgggaa cactaacagg cctccctgag tgagaacatt gcatgtgcgc 420
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acacaacagg gatagttcac ccaaaaaaca gaccattctt tttttctgtt gaacaaaaat 540
taagatattt tgaagaatgc ttaccgaata acttccatat ttggaaacta attacagtga 600
aagtcaatgg gtcttccagc attttttcaa tataccttac tttgagttca aaagaaaaac 660
acatctcaaa taggtttgag gttgaataaa catttttcat tttgggtgtg actatcccta 720
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atggttgaat ttatcttcat gtttatgtct gggttgtgct tttttgaaaa gatttccctg 840
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tcataacaac tccagttgat gccctttcac cctcagtgtg taaatatggc gtctgacatg 960
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ccagaatcat gtgtgaacg aagcctacca agagattttt gaaagccatc ggcttgacac 1080
gcgcacttct gatatctgtg gtatgttttg caaaagtgtc gctcagcctt tttagcatgg 1140
cagatcctcc acatcccac accctcctt caacctattc cctcctggaa agctatgtat 1200
ggggcgggaa gtgtaaatgg atatgggaag gaaggggggc accaccacac gctgccacct 1260
catctaggat gcctggggcc taaattgaag cctttcttac actaaacagg gcataagaga 1320
ccagcgcag ccaatcataa ttcagtgagc tctaaaatgg gccagccaat ggctgcagg 1380
gctagaggta tatatatcca aatcaaactc ttcttgcttg ggtgaccctc atttcggctt 1440
ggtgaacagg atccgg 1456

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<210> 9
 <211> 2205
 <212> DNA
 <213> Danio rerio

<220>
 <221> primer_bind
 <222> (2179)..(2205)
 <223> ARP2

<220>
 <221> misc_feature
 <222> (2153)..(2199)
 <223> Identical to the 5' ARP cDNA

<220>
 <221> intron
 <222> (792)..(2152)

<220>
 <221> misc_feature
 <222> (775)..(791)
 <223> Identical to the 5' ARP cDNA

<400> 9
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 attttaattt gtgttgtata attttacatt ttgtaagtat tatttttata aaaaatatat 120
 agaaataata caaatttggtt tacagtattc ttagttattg caataaacga attttatata 180
 gaaagagaaa gagttttatt ataagatgtt caatttaaaa aatggcagaa aatagaaaaa 240
 tgattgtcaa gatgataaaa gtcagtttag acaaaaaaat aagatgaaaa acatcaaaat 300
 agataataaa gtgacttttt tgggcggacc aaatttcctt attaatggc aattcattaa 360
 aatacattca ttaaaataaa ggtattgcga tgaatttaga tgcacagtga ttttggttct 420
 gtgcagattt ttggctgttg ttagaaggga tacatctgcg gccgaaagt aacgggaact 480
 atttacattc tttgctatta aattatccat tatttgtatt ttattacccc aaccgtaaac 540
 tcaaccctca cagtaatgta aaaatattat ttattgtttt atagcgtcac agaattgatc 600
 tatattgacc gcagctgtat cttttctaag tgcgactgta caaatacgca ctgaccgtga 660
 cagacacgtg cattgaccaa tcagcgcaca gatacgcat ttcgcgcga ttctgattgg 720
 atgatcgact gatactaata ttgtgccgtt tcctttcgcg gcctctttct ttcacgcgtc 780
 cctaccgtga ggtaaggctg acgccgctct tgtggcgggt tcttaaaatg tgtaataaaa 840
 taacatcata agaggtcacg agaaggctca cgtgtgttta atatcagcgg cggttattat 900
 tatgcgttta aagcttgtgt aatgattttt acagtaaaag ttagcactag cctgttagca 960
 caggcctcgt gcgccatgtg tgacgcgacg ttttaatatg atcttatttg attttgatga 1020
 tccgattctg atattaatca tatttatgctg taaaatgtgt gatgggtctg ctagtggaca 1080
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 tcaatcacat ataatttgtt ttatgtttta tttgagtcac cataccaggt aatagtttta 1260
 tttatattag tatgtacaat ttggcataaa ctgccttcgg ttttgattga catctacttt 1320
 gtaaagttaa tcttaaagggt gtaaaggctc acccaaaaga caattcacgg tcaagtgttt 1380
 tcaaattctt tgagtttctt aatgaacatg gtatgttttg gagaaaactg gaaaccaact 1440
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 ttcaaaatat ctacacaagt gtttaatgga aggaactcaa gtgatttgaa aagttaaggg 1560
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 taggcaacca aattacctgg aaacagttta caaacagtaa ttcataattt gtcatttaat 2100
 aagatgcaca caaggcaggt gtaaaagtat tgcttggtgt tgtaatcctc agattttaca 2160
 acctgtgtct taaaccggct gttcacccgat ccttgggaagg gatcc 2205

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Cytokeratin
 gene specific primer

<400> 10
 cgctggagta agagatagac ctgg 24

<210> 11
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Cytokeratin
 gene specific primer

<220>
 <221> misc_feature
 <222> (1)..(6)
 <223> Introduced for restriction site

<220>
 <221> misc_feature
 <222> (3)..(8)
 <223> BamHI site

<400> 11
 ccggatcctg tgtctttgag ttgctg 26

<210> 12
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Muscle
 creatine kinase gene specific primer

<220>
 <221> misc_feature
 <222> (3)..(8)
 <223> BamHI site

<400> 12
ccggatcctt gggatcagat cctg

24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Muscle
creatine kinase gene specific primer

<220>
<221> misc_feature
<222> (1)..(3)
<223> Introduced for restriction site

<220>
<221> misc_feature
<222> (3)..(8)
<223> BamHI site

<400> 13
ccggatcctg ttcaccaagc cgaa

24

<210> 14
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<400> 14
tagttggact tccacgtgcc ctgtc

25

<210> 15
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Acidic
ribosomal protein PO gene specific primer

<220>
<221> misc_feature
<222> (1)..(7)
<223> Introduced for restriction site

<220>
<221> misc_feature

<222> (1)..(6)
<223> BamHI site

<400> 15
ggatcccttc caaggatcgg tgaaca

26

<210> 16
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<400> 16
gttcacatcttt acaagctagc gctgaacaat gctgtggaca agcttgaatt c

51

<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide for linker used in linker-mediated
PCR

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a dideoxycytidine

<400> 17
gaattcaagn

10

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: linker
specific primer

<400> 18
gttcacatcttt acaagctagc g

21

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: linker
 specific primer

<400> 19
 tcctgaacaa tgctgtggac

20

<210> 20
 <211> 1392
 <212> DNA
 <213> Danio rerio

<220>
 <221> CDS
 <222> (42)..(551)

<220>
 <221> primer_bind
 <222> (6)..(28)
 <223> M2

<220>
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 <222> (23)..(45)
 <223> M1

<220>
 <221> polyA_signal
 <222> (797)..(802)

<220>
 <221> polyA_signal
 <222> (1351)..(1357)

<400> 20
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 Met Ala Pro Lys Lys
 1 5

gcc aag agg agg gca gca gga gga gag ggt tcc tcc aac gtc ttc tcc 104
 Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser Ser Asn Val Phe Ser
 10 15 20

atg ttt gag cag agc cag att cag gag tac aaa gag gct ttc aca atc 152
 Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys Glu Ala Phe Thr Ile
 25 30 35

att gac cag aac aga gac ggt atc atc agc aaa gac gac ctt agg gac 200
 Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys Asp Asp Leu Arg Asp
 40 45 50

gtg ttg gcc tca atg ggc cag ctg aat gtg aag aat gag gag ctg gag 248
 Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys Asn Glu Glu Leu Glu
 55 60 65

gcc atg atc aag gaa gcc agc ggc cca atc aac ttc acc gtt ttc ctc 296
Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn Phe Thr Val Phe Leu
70 75 80 85

acc atg ttc gga gag aag ttg aag ggt gct gac ccc gaa gac gtc atc 344
Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp Pro Glu Asp Val Ile
90 95 100

gtg tct gcc ttc aag gtg ctg gac cct gag ggc act gga tcc atc aag 392
Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly Thr Gly Ser Ile Lys
105 110 115

aag gaa ttc ctt gag gag ctt ttg acc act cag tgc gac agg ttc acc 440
Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln Cys Asp Arg Phe Thr
120 125 130

gca gag gag atg aag aat ctg tgg gcc gcc ttc ccc cca gat gtg gct 488
Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe Pro Pro Asp Val Ala
135 140 145

ggc aat gtt gac tac aag aac atc tgc tac gtc atc aca cac gga gag 536
Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val Ile Thr His Gly Glu
150 155 160 165

gag aag gag gag taa acaaccttgg aatcaagaaa acgaagagaa gaacatgcat 591
Glu Lys Glu Glu

cctcacagct taatctccag tctgttgtct ggctttctct aacttttgtt tttccttct 651
ccctttcttg ctttctacca tcgttggttac tccaagcact tacactctcc atcttacc 711
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cctcttctct atttctctgt ccattctttt ttttttcttt tttctttttt gctttctgca 1311
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aataaaaaaa aaaaaaaaaa a 1392

<210> 21
<211> 169
<212> PRT
<213> Danio rerio

<400> 21
Met Ala Pro Lys Lys Ala Lys Arg Arg Ala Ala Gly Gly Glu Gly Ser
1 5 10 15

Ser Asn Val Phe Ser Met Phe Glu Gln Ser Gln Ile Gln Glu Tyr Lys
20 25 30

Glu Ala Phe Thr Ile Ile Asp Gln Asn Arg Asp Gly Ile Ile Ser Lys
35 40 45

Asp Asp Leu Arg Asp Val Leu Ala Ser Met Gly Gln Leu Asn Val Lys
50 55 60

Asn Glu Glu Leu Glu Ala Met Ile Lys Glu Ala Ser Gly Pro Ile Asn
65 70 75 80

Phe Thr Val Phe Leu Thr Met Phe Gly Glu Lys Leu Lys Gly Ala Asp
85 90 95

Pro Glu Asp Val Ile Val Ser Ala Phe Lys Val Leu Asp Pro Glu Gly
100 105 110

Thr Gly Ser Ile Lys Lys Glu Phe Leu Glu Glu Leu Leu Thr Thr Gln
115 120 125

Cys Asp Arg Phe Thr Ala Glu Glu Met Lys Asn Leu Trp Ala Ala Phe
130 135 140

Pro Pro Asp Val Ala Gly Asn Val Asp Tyr Lys Asn Ile Cys Tyr Val
145 150 155 160

Ile Thr His Gly Glu Glu Lys Glu Glu
165

<210> 22
<211> 2054
<212> DNA
<213> Danio rerio

<220>
<221> TATA_signal
<222> (1983)..(1989)

<220>
<221> enhancer
<222> (142)..(148)
<223> E-box, canntg

<220>
<221> enhancer
<222> (452)..(457)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1095)..(1100)
<223> E-box, canntg

<220>
<221> enhancer
<222> (1278)..(1283)
<223> E-box, canntg

<220>
<221> enhancer

<222> (1362)..(1367)
 <223> E-box, canntg

 <220>
 <221> enhancer
 <222> (1385)..(1390)
 <223> E-box, canntg

 <220>
 <221> enhancer
 <222> (523)..(532)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <221> enhancer
 <222> (606)..(615)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <221> enhancer
 <222> (697)..(706)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <221> enhancer
 <222> (1490)..(1499)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <221> enhancer
 <222> (1640)..(1649)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <221> enhancer
 <222> (1956)..(1965)
 <223> Potential MEF2 binding site, yta(w)4tar

 <220>
 <223> Transcription start site at residue 2012

 <220>
 <221> primer_bind
 <222> (2032)..(2054)
 <223> M2

 <220>
 <221> misc_difference
 <222> (2027)..(2054)
 <223> Identical to the 5' MLC2f cDNA

<400> 22
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 gtggacagct tgaattcaat tcgccacaga ggaatgagcc accaactcat ccagtgtatt 120
 ttttatgcag cggatgccca tccagttgca accctacact gggaaacacc caaatctgtc 180
 ttttaaatta atatttttaa taggaagcta tggttatatt gtgcataaac attagattag 240
 tcagtacact ctcaaaaata aatgggtccgc aagctgtcac tgcggtggtg ccttttcaaa 300

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aggtacatat ttgtacttaa aggggtccata ttgatacctc aaaagtatat attagtgcct 360
aaaaatttta agagaaacac ttttgtactt tttagggtact aatatatacc cttgagggtt 420
tattatggac ctttaaggta caaattttta tcatttggaa aggtaccacc ccagtgcacag 480
ctcacgccct ttatttctga gagtgaagct aaatctggag cttatttaac aaaataactt 540
atgataacgg tccaaaaact actacacca tatttatatg ttattgaaaa atattaaata 600
caaatttata aacaggggaa aatcaagaga agcaaaacaa tggaaaaaaa ttagttcaaa 660
attttaggtg tgtaattttt ttgttgcaat atttagcttt atttaaattg ttttatcttt 720
caattttgtg actaaaatat tattttaata aatatagctg ttaataaat ctgttttgtt 780
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